

See sheet For Case

5/3/06

TO: Ms. Patricia Booker, PCT DO/EO

FROM: Anne-Marie Corrigan, STIC

Per your request, please find copy of non-errored raw sequence listing for 10/516558.

Please contact me if you have any questions.

Thank you.

Total pages (including cover sheet): 9

*re-run***RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/516,558A
Source: PG
Date Processed by STIC: 3/9/06

ENTERED

re-run

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 05/03/2006
TIME: 15:20:20Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\05032006\J516558A.raw

3 <110> APPLICANT: Chano, Tokuhiro
4 Okabe, Hidetoshi
5 Ikegawa, Shiro
7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
9 <130> FILE REFERENCE: 3190-070
11 <140> CURRENT APPLICATION NUMBER: US 10/516,558A
12 <141> CURRENT FILING DATE: 2004-11-30
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00682
15 <151> PRIOR FILING DATE: 2003-01-30
17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
18 <151> PRIOR FILING DATE: 2002-06-03
20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
21 <151> PRIOR FILING DATE: 2002-07-24
23 <160> NUMBER OF SEQ ID NOS: 132
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1594
29 <212> TYPE: PRT
30 <213> ORGANISM: Unknown
32 <220> FEATURE:
33 <223> OTHER INFORMATION: human RB1CC1
35 <400> SEQUENCE: 1
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38 1 5 10 15
41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
42 20 25 30
45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
46 35 40 45
49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
50 50 55 60
53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
54 65 70 75 80
57 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
58 85 90 95
61 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
62 100 105 110
65 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
66 115 120 125
69 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
70 130 135 140
73 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
74 145 150 155 160
77 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser

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78 165 170 175
81 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
82 180 185 190
85 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
86 195 200 205
89 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
90 210 215 220
93 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
94 225 230 235 240
97 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
98 245 250 255
101 Ser Phe Pro Lys Ser Val Gln His Val Ser Pro Asp Thr Ala Asp Ala
102 260 265 270
105 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
106 275 280 285
109 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
110 290 295 300
113 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp
114 305 310 315 320
117 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp
118 325 330 335
121 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala
122 340 345 350
125 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg
126 355 360 365
128 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn
129 370 375 380
132 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala
133 385 390 395 400
136 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His
137 405 410 415
140 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp
141 420 425 430
144 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu
145 435 440 445
148 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln
149 450 455 460
152 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu
153 465 470 475 480
156 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr
157 485 490 495
160 Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His
161 500 505 510
164 Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr
165 515 520 525
168 Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys
169 530 535 540
172 Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro
173 545 550 555 560

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176 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
177 565 570 575
180 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
181 580 585 590
184 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
185 595 600 605
188 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
189 610 615 620
191 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
192 625 630 635 640
195 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
196 645 650 655
199 Glu Ser Thr Ala Gly Ile Thr Thr Thr Thr Ser Pro Arg Thr Pro Pro
200 660 665 670
203 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
204 675 680 685
207 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
208 690 695 700
211 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
212 705 710 715 720
215 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
216 725 730 735
219 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
220 740 745 750
223 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
224 755 760 765
227 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly
228 770 775 780
231 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg
232 785 790 795 800
235 Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys
236 805 810 815
239 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp
240 820 825 830
243 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile
244 835 840 845
247 Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln
248 850 855 860
251 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly
252 865 870 875 880
254 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys
255 885 890 895
258 Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu
259 900 905 910
262 Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn
263 915 920 925
266 Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln
267 930 935 940
270 Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu

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271 945 950 955 960
274 Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu Gln Leu Leu
275 965 970 975
278 Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu
279 980 985 990
282 Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr
283 995 1000 1005
286 Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln
287 1010 1015 1020
290 Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu
291 1025 1030 1035
294 Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu
295 1040 1045 1050
298 Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu
299 1055 1060 1065
302 Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala
303 1070 1075 1080
306 Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu
307 1085 1090 1095
310 Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp
311 1100 1105 1110
314 Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu
315 1115 1120 1125
317 Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg
318 1130 1135 1140
321 His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val
322 1145 1150 1155
325 Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys
326 1160 1165 1170
329 Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser
330 1175 1180 1185
333 Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu
334 1190 1195 1200
337 Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys
338 1205 1210 1215
341 Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys
342 1220 1225 1230
345 Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu
346 1235 1240 1245
349 Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys
350 1250 1255 1260
353 Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp
354 1265 1270 1275
357 Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu
358 1280 1285 1290
361 Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu
362 1295 1300 1305
365 Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser
366 1310 1315 1320

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369 Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg
370 1325 1330 1335
373 Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys
374 1340 1345 1350
377 Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile
378 1355 1360 1365
381 Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys
382 1370 1375 1380
385 Lys Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val
386 1385 1390 1395
389 Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys
390 1400 1405 1410
393 Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr
394 1415 1420 1425
397 Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
398 1430 1435 1440
401 Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
402 1445 1450 1455
405 Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Glu Asn
406 1460 1465 1470
409 Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
410 1475 1480 1485
413 Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
414 1490 1495 1500
417 Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
418 1505 1510 1515
421 Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
422 1520 1525 1530
425 Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
426 1535 1540 1545
429 Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
430 1550 1555 1560
433 Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
434 1565 1570 1575
437 Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
438 1580 1585 1590
441 Val
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447 <211> LENGTH: 1588
448 <212> TYPE: PRT
449 <213> ORGANISM: Unknown
451 <220> FEATURE:
452 <223> OTHER INFORMATION: mouse Rblcc1
454 <400> SEQUENCE: 2
456 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
457 1 5 10 15
460 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
461 20 25 30
464 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/516,558A

DATE: 05/03/2006
TIME: 15:20:21

Input Set : A:\3190-070 Sequence Listing.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
Seq#:55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78
Seq#:79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101
Seq#:102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119
Seq#:120,121,122,123,124,125,126,127,128,129,130,131,132

VERIFICATION SUMMARY

DATE: 05/03/2006

PATENT APPLICATION: US/10/516,558A

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